



**Amendments to the Specification:**

Please replace the "Reference to Related Applications" section with the following amended paragraphs:

**The present application includes the subject of Provisional Application Serial No. 60/455,563 filed March 19, 2003 and claims the priority thereof.**

**The present application is a continuation in part of US Patent Application Serial Number 09/866,925 filed May 30, 2001 entitled ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES[[.]] (referred to as "basic methods patent application"); and claims the priority thereof.**

**This present application is related to PCT application PCT/US01/16471 filed May 31, 2001 and entitled ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES.**

**The present application is also related to US Patent Application Serial Number 10/339,666 filed January 10, 2003 entitled SIMULATION OF GENE EXPRESSION CONTROL USING CONNECTRONS, INTERFERENCE RNAS (IRNAS) AND SMALL TEMPORAL RNAS (STRNAS) IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES**

The present application is also related to US Patent Application Serial Number 10/364,516 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE ESCHERICHIA COLI K-12 MG1655 COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/364,412 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE SACCHAROMYCES CEREVISIAE COMPLETE GENOME, ~~and applicant claims the priority of each of the above identified pending applications.~~

On page 3, please replace the two sections entitled "**Reverse Complement**" and "**Equivalent Sequences**" (at actual lines 3-15) with the following amended sections thereof:

**Reverse Complement** - Going away from a given point, the same sequence occurs on opposite strands. In the example below the sequence GCATCC in the dominant direction of the positive strand occurs somewhere else in the genome in the anti-dominant direction of the negative strand

Positive Strand  
SEQ ID No. 121

5'- **GCATCC**GTGTAAT ATTACACGGATGC -3'

Negative Strand  
SEQ ID No. 122

3'- CGTAGGCACATTA **TAATGTGCCTACG** -5'

**Equivalent Sequences** - Two sequences such that the second sequence is in the reverse complement of the first sequence

First sequence

SEQ ID No. 123

5'- GCATCCGTGTAAT -3' (A)

Second sequence

SEQ ID No. 124

5'- ATTACACGGATGC -3' (A')

If the first sequence is called A then the second sequence is called A'

Please replace the entire "Examples" section which begins on at the top of page 21 and ends at the end of page 46 with the following amended section (26 pages):

Figures 1 to 14 provide a large number of ways of describing and designing connectron pairs in a genome. We give examples of the description of symmetric and asymmetric connectron pairs in six classes of genomes (prokaryotic, Archeal, single-celled eukaryotic, multi-celled eukaryotic, mammalian and plant). We also give two examples of the design of an asymmetric connectron pair in a single-celled eukaryote and a mammal. It is clear that many other variations of symmetric and asymmetric connectron pairs could be described or designed by someone skilled in the art.

**Description of a symmetric lower-upper connectron pair in *E. coli***

*E. coli* is a prokaryotic organism. A single connectron has been selected from the *E. coli* connectrome to illustrate the properties of a lower-upper connectron pair. Because the connectron is very long it can be split into two connectrons that then bind as a pair. In this and each of the following examples, a header indicates the function of each data field. Because of print-page limitations, the "sequence of match" field has been moved to the left side of each example.

The connectron 1434 has a C1-T1 binding length of 182 bases and a C2-T2 binding length of 171 bases. The shorter of the two matches of 171 bases is then halved with the first half becoming the A and the second half becoming the B in figure 3a producing a producted connectron pair lifetime of 7225.

genome  
Connectron id  
chromosome  
contig  
(.groups) id  
type  
CP = control element on positive strand  
CN = control element on negative strand  
TP = target element on positive strand  
TN = target element on negative strand  
match start  
match stop  
type of Connectron  
l/u = lower/upper  
l/r = left/right  
source of Connectron  
g = gene  
p = pseudogene  
length of match  
sequence of match  
eco 1434 1 1 7435 CP 4505.026 4505.207 l/u g 182

25 SEQ ID No. 125 CTGTAGATTCAATCTGTCAATGCAACACCCCTTTCAATTATCTCTTTCGG  
TGTTTTGAACTTCAGTGTCTTTCTCGGTCTGTTGTTTAGCTGAGCAGCAA  
CCAGATCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGA  
AAGTACTGCCGAATTAGCCCATTTGTGTTCTC  
eco 1434 1 1 508 TN 279.155 279.336 l/u g 182

30 SEQ ID No. 126 CTGTAGATTCAATCTGTCAATGCAACACCCCTTTCAATTATCTCTTTCGG  
TGTTTTGAACTTCAGTGTCTTTCTCGGTCTGTTGTTTAGCTGAGCAGCAA  
CCAGATCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGA  
AAGTACTGCCGAATTAGCCCATTTGTGTTCTC  
eco 1434 1 1 7435 CP 4505.031 4505.201 l/u g 171

35 SEQ ID No. 127 GATTCAATCTGTCAATGCAACACCCCTTTCAATTATCTCTTTCGGTGTTT  
TGAATTCAGTGTCTTTCTCGGTCTGTTGTTTAGCTGAGCAGCAACCAGA  
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA  
CTGCCGAATTAGCCCATTTGT  
40 eco 1434 1 1 472 TN 270.811 270.981 l/u g 171

45 SEQ ID No. 128 GATTCAATCTGTCAATGCAACACCCCTTTCAATTATCTCTTTCGGTGTTT  
TGAATTCAGTGTCTTTCTCGGTCTGTTGTTTAGCTGAGCAGCAACCAGA  
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA  
CTGCCGAATTAGCCCATTTGT

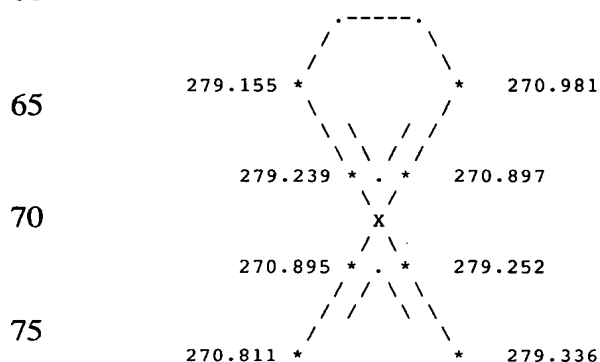
Can form an AB symmetric pair of l/u Connectrons with a lifetime =  $85 \times 85 = 7225$   
171

50 SEQ ID No. 129 GATTCAATCTGTCAATGCAACACCCCTTTCAATTATCTCTTTCGGTGTTT  
TGAATTCAGTGTCTTTCTCGGTCTGTTGTTTAGCTGAGCAGCAACCAGA  
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA  
CTGCCGAATTAGCCCATTTGT

171

55 SEQ ID No. 130 GATTCAATCTGTCAATGCAACACCCCTTTCAATTATCTCTTTCGGTGTTT  
TGAATTCAGTGTCTTTCTCGGTCTGTTGTTTAGCTGAGCAGCAACCAGA  
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA  
CTGCCGAATTAGCCCATTTGT

60 279.155 279.239 279.252 279.336 --- 270.811 270.895 270.897 270.981



**Description of a symmetric lower-upper connectron pair  
in *S. tokodaii***

*S. tokodaii* is a Archeal organism. In this and the following  
5 examples, the header does not show all the cases for a given  
data field.

The connectron 4240 has a C1-T1 binding length of 67 bases and a  
C2-T2 binding length of 85 bases. The effective match of 52  
10 bases is then halved with the first half becoming the A and the  
second half becoming the B in figure 3a producing a producted  
connectron pair lifetime of 676.

15 genome  
Connectron id  
chromosome  
contig  
(.groups) id  
type  
match start  
match stop  
type of Connectron  
source of Connectron  
length of match  
sto 4240 1 1 3986 CN 1178.996 1179.062 1/u g 67

30 SEQ ID No. 131 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTTCTCCCTTGAATA  
AACTACCGGGTACATGA

sto 4240 1 1 447 TP 61.903 61.969 1/u g 67

35 SEQ ID No. 132 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTTCTCCCTTGAATA  
AACTACCGGGTACATGA

40 sto 4240 1 1 3986 CN 1178.963 1179.047 1/u g 85

SEQ ID No. 133 TTGTAATATTATATCAGTTTACTTCTAATATACTGTACCCCTTCAAGTA  
AGCCTCATTTAAGGGAGTTTTCTCCCTTGAATAAA

45 sto 4240 1 1 646 TP 123.599 123.683 1/u g 85

SEQ ID No. 134 TTGTAATATTATATCAGTTTACTTCTAATATACTGTACCCCTTCAAGTA  
AGCCTCATTTAAGGGAGTTTTCTCCCTTGAATAAA

50

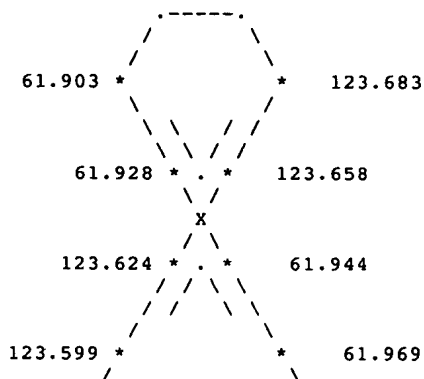
Can form an AB symmetric pair of 1/u Connectrons with a lifetime = 26 X 26 = 676

52

SEQ ID No. 135 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTCTCCCTTGAATA  
AA

SEQ ID No. 136 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTCTCCCTTGAATA  
AA

61.903 61.928 61.944 61.969 --- 123.599 123.624 123.658  
123.683



**Description of a symmetric lower-upper connectron pair  
in *S. cerevisiae***

The connectron 385 has a C1-T1 binding length of 117 and a C2-T2  
binding length also of 117 bases. Since the two matches are  
equal, the 117 bases are then halved with the first half  
becoming the A and the second half becoming the B in figure 3a  
producing a producted connectron pair lifetime of 3364.

*S. cerevisiae* is a single-celled eukaryotic organism.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match										
yst	385	15	15	28455	CP	975.950	976.066	1/u	g	117

SEQ ID No. 137 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG  
AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA  
ATAGGATCAATGAATAT

yst 385 1 1 419 TN 165.888 166.004 1/u g 117

SEQ ID No. 138 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG  
AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA  
ATAGGATCAATGAATAT

yst 385 15 15 28455 CP 975.950 976.066 1/u g 117

SEQ ID No. 139 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG



AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA  
 ATAGGATCAATGAATAT

5                    yst            385            1            1            355 TN            160.257            160.373 1/u g            117

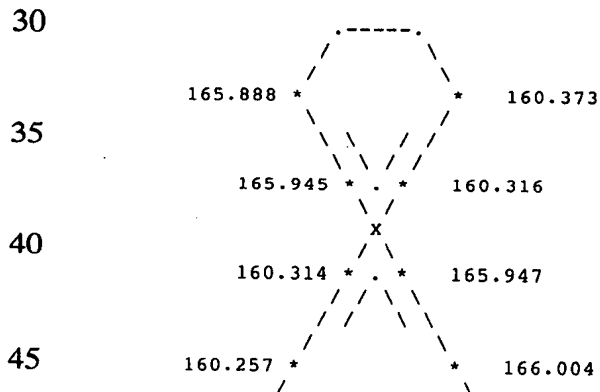
10                    SEQ ID No. 140    TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG  
                      AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA  
                      ATAGGATCAATGAATAT

15                    Can form an AB symmetric pair of 1/u Connectrons with a lifetime =  $58 \times 58 = 3364$

SEQ ID No. 141    TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG  
                      AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA  
                      ATAGGATCAATGAATAT

20                    SEQ ID No. 142    TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG  
                      AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA  
                      ATAGGATCAATGAATAT

25                    165.888 165.945 165.947 166.004 --- 160.257 160.314 160.316 160.373



50    **Description of a symmetric lower-upper connectron pair  
 in *C. elegans***

*C. elegans* is a 1,000-celled eukaryotic organism.

55    The connectron 55 has a C1-T1 binding length of 68 and a C2-T2  
 binding length also of 68 bases. The effective match of 43  
 bases is then halved with the first half becoming the A and the  
 second half becoming the B in figure 3a producing a produced  
 connectron pair lifetime of 441.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
wrm	55	1	1	380	CN	221.205	221.272	1/u	g	68

SEQ ID No. 143 GGG AATTGCTTCGTCAAATGATCGACGGAGGGCTTTGGCCATCTGCAAG  
GATAAACTCGCATGTCGA

wrm 55 1 1 433 TN 250.979 251.046 1/u g 68

SEQ ID No. 144 GGG AATTGCTTCGTCAAATGATCGACGGAGGGCTTTGGCCATCTGCAAG  
GATAAACTCGCATGTCGA

wrm 55 1 1 380 CN 221.180 221.247 1/u g 68

SEQ ID No. 145 GAGCTCGCAACACCGGCCGAGCAGCGGAATTGCTTCGTCAAATGATCGA  
CGGAGGGCTTTTGGCCAT

wrm 55 1 1 354 TN 214.904 214.971 1/u g 68

SEQ ID No. 146 GAGCTCGCAACACCGGCCGAGCAGCGGAATTGCTTCGTCAAATGATCGA  
CGGAGGGCTTTTGGCCAT

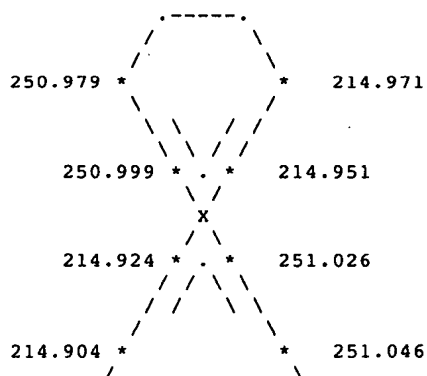
Can form an AB symmetric pair of 1/u Connectrons with a lifetime =  $21 \times 21 = 441$   
43

SEQ ID No. 147 GGG AATTGCTTCGTCAAATGATCGACGGAGGGCTTTTGGCCAT

43

SEQ ID No. 148 GGG AATTGCTTCGTCAAATGATCGACGGAGGGCTTTTGGCCAT

250.979 250.999 251.026 251.046 --- 214.904 214.924 214.951 214.971

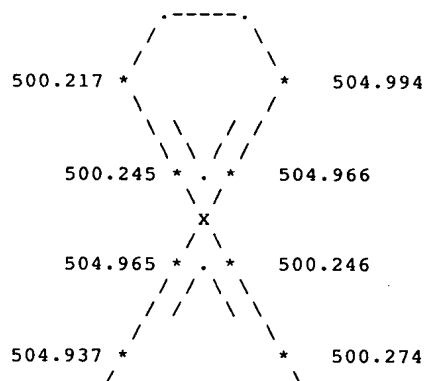


**Description of a symmetric lower-upper connectron pair in *H. sapiens***

*H. sapiens* is a multi-celled eukaryotic organism - a mammal.

The connectron 1211 has a C1-T1 binding length of 58 bases and a C2-T2 binding length also of 58 bases. Since the two matches are equal, 58 is then halved with the first half becoming the A and the second half becoming the B in figure 3a producing a producted connectron pair lifetime of 841.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match									
hsd	1211	4	1	1331 CP	16.381	16.438	l/u g		58
<u>SEQ ID No. 149</u> GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT									
AAAGATCA									
hsd	1211	4	1	1542 TP	500.217	500.274	l/u g		58
<u>SEQ ID No. 150</u> GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT									
AAAGATCA									
hsd	1211	4	1	1331 CP	16.381	16.438	l/u g		58
<u>SEQ ID No. 151</u> GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT									
AAAGATCA									
hsd	1211	4	1	1559 TP	504.937	504.994	l/u g		58
<u>SEQ ID No. 152</u> GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT									
AAAGATCA									
Can form an AB symmetric pair of l/u Connectrons with a lifetime = $29 \times 29 = 841$									
<u>SEQ ID No. 153</u> GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT									
AAAGATCA									
<u>SEQ ID No. 154</u> GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT									
AAAGATCA									
500.217	500.245	500.246	500.274	---	504.937	504.965	504.966	504.994	



# **Description of a symmetric lower-upper connectron pair in *A. thaliana***

*A. thaliana* is a multi-celled eukaryotic organism - a plant.

The connectron 3 has a C1-T1 binding length of 94 bases and a C2-T2 binding length of 79 bases. The shorter of the two matches of 79 bases is then halved with the first half becoming

the A and the second half becoming the B in figure 5a producing a producted connectron pair lifetime of 1521.

[illegible]

SEQ ID No. 155 TGTGAAAGTTAAACTTGATTTTGAATCAAGTTAATTATTGGATCAATT  
ATCCAATAATTAATTAAGGCCAAATCCAAGTTCTAGAGTTTCT

ath	3	1	1	7951 TP	3780.765	3780.858	1/u q	94
-----	---	---	---	---------	----------	----------	-------	----

SEQ ID No. 156 TGGTGAAGTGTAAACTTGATTTGAATCAAGTTTAATTATTGGATCAATT  
ATCCAATAATTAATTTATGGCCAAATCCAAGTTCTAGAGTTTTCCT

ath	3	5	1	29822 CN	21590.870	21590.950	1/u g	79
-----	---	---	---	----------	-----------	-----------	-------	----

SEQ ID No. 157 TGGTGAAGTAAACTTGATTTGAATCAAGTTAATTATTGGATCAATT  
ATCCAATAATTAATTATGCCCAAATCCAA

ath	3	1	1	7985 TP	3785.281	3785.359	1/u g	79
-----	---	---	---	---------	----------	----------	-------	----

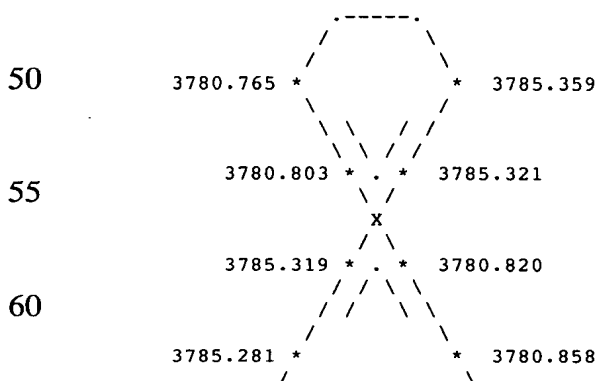
SEQ ID No. 158 TGTGTGAAGTTAAACTTGATTTTGAATCAAGTTTAATTATTGGATCAATT  
ATCCAATAATTAATTATGCCCAAATCCAA

Can form an AB symmetric pair of 1/u Connectrons with a lifetime =  $39 \times 39 = 1521$

SEQ ID No. 159 TGTGTAAAGTTAAACTTGATTTGAATCAAGTTTAATTATTGGATCAATT  
ATCCAATAATTAAATTATGGCCAAATCCAA

SEQ ID No. 160 TGGTTGAAAGTTAAACTTGATTTGAATCAAGTTAATTATTGGATCAATT  
ATCCAATAATTAATTATGGCCAAATCCAA

45	3785.359	3780.765	3780.803	3780.820	3780.858 ---	3785.281	3785.319	3785.321
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65 Description of an asymmetric lower-upper connectron pair in *E. coli*

The connectron 14918 has a C1-T1 binding length of 27 bases and a C2-T2 binding length of 35 bases. The shorter of the two matches at 27 bases produces the lifetime for this connectron. The connectron 15118 has a C1-T1 binding length of 20 bases and

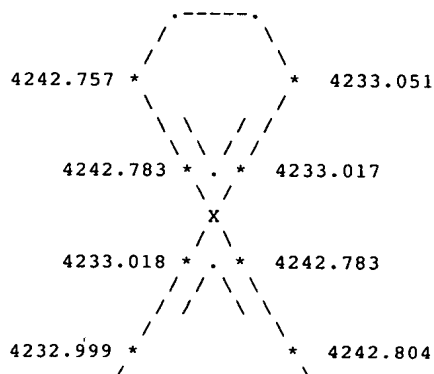
a C2-T2 binding length of 22 bases. The shorter of the two matches at 20 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 9d is 540.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match									
eco 14918	1	1	7316 CN	4454.807	4454.833	1/u g		27	
<u>SEQ ID No. 161</u>									
eco 14918	1	1	6955 TN	4242.757	4242.783	1/u g		27	
<u>SEQ ID No. 162</u>									
eco 14918	1	1	7316 CN	4454.810	4454.844	1/u g		35	
<u>SEQ ID No. 163</u>									
eco 14918	1	1	6937 TN	4233.017	4233.051	1/u g		35	
<u>SEQ ID No. 164</u>									
eco 15118	1	1	1544 CP	831.575	831.594	1/u g		20	
<u>SEQ ID No. 165</u>									
eco 15118	1	1	6939 TP	4232.999	4233.018	1/u g		20	
<u>SEQ ID No. 166</u>									
eco 15118	1	1	1544 CP	831.596	831.617	1/u g		22	
<u>SEQ ID No. 167</u>									
eco 15118	1	1	6957 TP	4242.783	4242.804	1/u g		22	
<u>SEQ ID No. 168</u>									

Found L/U AD AB - CD Connectron pair for 14918 and 15118 with a lifetime = 27 X 20 = 540

.000 .001

4242.757 4242.783 4233.017 4233.051 --- 4232.999 4233.018 4242.783 4242.804



# Description of an asymmetric lower-upper connectron pair in *S. tokodaii*

The connectron 6416 has a C1-T1 binding length of 59 bases and a C2-T2 binding length of 60 bases. The shorter of the two matches at 59 bases produces the lifetime for this connectron. The connectron 6477 has a C1-T1 binding length of 189 bases and a C2-T2 binding length of 36 bases. The shorter of the two matches at 36 bases produces the lifetime for this connectron. The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 9d is 2124.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sto	6416	1	1	3245 CP	1036.523	1036.581	1/u g		59

SEQ ID No. 169 ACTCCCAGTGAGGGATAGGGGTAACGGACTGAAGACCCAGCCCGTGGTCT

ACCGCTGGA

sto	6416	1	1	3439 TP	1079.594	1079.652	1/u g	59
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 170 ACTCCCAGTGAGGGATAGGGGTAACGGACTGAAGACCCAGCCCGTGGTCT

ACCGCTGGA

sto	6416	1	1	3250 CP	1036.635	1036.694	1/u g	60
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 171 ATGAAGGTGGTAAACCACAAACCTATGAACCGCCCTAAGGGAACCCCTCGC

CCTTTAGGGC

sto	6416	1	1	3714 TP	1146.360	1146.419	1/u g	60
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 172 ATGAAGGTGGTAAACCACAAACCTATGAACCGCCCTAAGGGAACCCCTCGC

CCTTTAGGGC

sto	6477	1	1	618 CN	120.361	120.549	1/u g	189
-----	------	---	---	--------	---------	---------	-------	-----

SEQ ID No. 173 CTATCCCTCACCAAGAGTTGCCCTCTGCTCTTGGCTCTTGGGGACTCGGG

GATATGTAGTTCTGTGCGGGACACATATCTTCAGTATGCCCACCTTTGT

GGGCTTCCCCGCACTTTATTAATAGTTTAAAGCTAAGATTAAAACTTTA

CCCCGCCTTAAAGGCGAGGCTTGCCCCGCGTTTGTCA

sto	6477	1	1	3709 TN	1146.169	1146.357	1/u g	189
-----	------	---	---	---------	----------	----------	-------	-----

SEQ ID No. 174 CTATCCCTCACCAAGAGTTGCCCTCTGCTCTTGGCTCTTGGGGACTCGGG

GATATGTAGTTCTGTGCGGGACACATATCTTCAGTATGCCCACCTTTGT

GGGCTTCCCCGCACTTTATTAATAGTTTAAAGCTAAGATTAAAACTTTA

CCCCGCCTTAAAGGCGAGGCTTGCCCCGCGTTTGTCA

sto	6477	1	1	622 CN	120.590	120.625	1/u g	36
-----	------	---	---	--------	---------	---------	-------	----

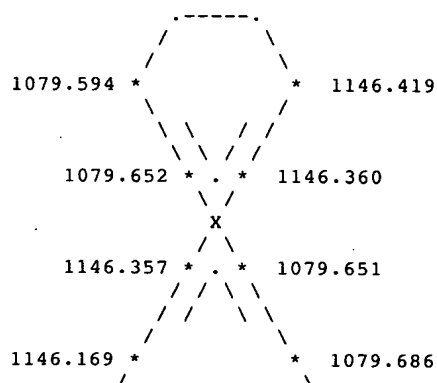
SEQ ID No. 175 CACCCACCCGCTCCGTTTCGTCCAGCGGTAGACCAC

sto	6477	1	1	3446 TN	1079.651	1079.686	1/u g	36
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 176 CACCCACCCGCTCCGTTTCGTCCAGCGGTAGACCAC

.001 .003

1079.594 1079.652 1146.360 1146.419 --- 1146.169 1146.357 1079.651 1079.686



**Description of an asymmetric lower-upper connectron pair  
in *S. cerevisiae***

The connectron 3814 has a C1-T1 binding length of 72 bases and a C2-T2 binding length of 72 bases. The either of the two matches at 72 bases produces the lifetime for this connectron. The connectron 3847 has a C1-T1 binding length of 81 bases and a C2-T2 binding length of 89 bases. The shorter of the two matches at 81 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 9d is 5832.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match				type					
yst	3814	13	13	23498 CP	362.701	362.772	1/u g		72

SEQ ID No. 177 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT  
TTTATATGTTTCATTATCCTAT

yst	3814	2	2	1896 TN	265.267	265.338	1/u g		72
-----	------	---	---	---------	---------	---------	-------	--	----

SEQ ID No. 178 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT  
TTTATATGTTTCATTATCCTAT

yst	3814	13	13	23498 CP	362.701	362.772	1/u g		72
-----	------	----	----	----------	---------	---------	-------	--	----

SEQ ID No. 179 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT  
TTTATATGTTTCATTATCCTAT

yst	3814	2	2	1495 TN	226.820	226.891	1/u g		72
-----	------	---	---	---------	---------	---------	-------	--	----

SEQ ID No. 180 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT  
TTTATATGTTTCATTATCCTAT

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yst	3847	13	13	23551 CN	372.772	372.852	1/u g	81
-----	------	----	----	----------	---------	---------	-------	----

5 SEQ ID No. 181 AAACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAAT  
ATAGATTCCATTTTGAGGATTCCTATATCCT

yst	3847	2	2	1496 TP	226.739	226.819	1/u g	81
-----	------	---	---	---------	---------	---------	-------	----

10 SEQ ID No. 182 AAACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAAT  
ATAGATTCCATTTTGAGGATTCCTATATCCT

yst	3847	13	13	23551 CN	372.836	372.924	1/u g	89
-----	------	----	----	----------	---------	---------	-------	----

15 SEQ ID No. 183 GAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTA  
ATATTATAGCCTTTATCAACAATGGAATCCCAACAATTA

yst	3847	2	2	1923 TP	265.340	265.428	1/u g	89
-----	------	---	---	---------	---------	---------	-------	----

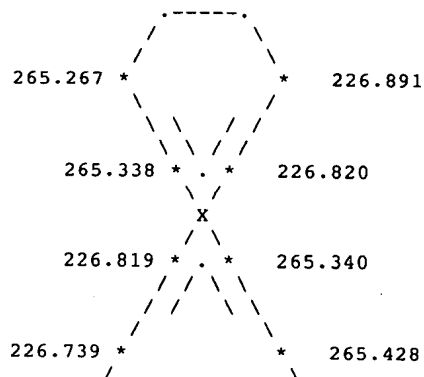
20 SEQ ID No. 184 GAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTA  
ATATTATAGCCTTTATCAACAATGGAATCCCAACAATTA

-----

25 Found L/U AD AB - CD Connectron pair for 3814 and 3847 with a lifetime = 72 X 81 = 5832

.002 .001

30 265.267 265.338 226.820 226.891 --- 226.739 226.819 265.340 265.428



50 **Description of an asymmetric lower-upper connectron pair  
in *C. elegans***

The connectron 23175 has a C1-T1 binding length of 15 bases and  
55 a C2-T2 binding length of 18 bases. The shorter of the two  
matches at 15 bases produces the lifetime for this connectron.

The connectron 23179 has a C1-T1 binding length of 16 bases and  
a C2-T2 binding length of 19 bases. The shorter of the two  
matches at 16 bases produces the lifetime for this connectron.

60 The lifetime of this pair of dominant - anti-dominant  
connectrons as shown in figure 9c is 240.



genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match				type					
wrm	23175	4	2	22854 CP	708.778	708.792	1/u g		15

SEQ ID No. 185

TGGTCTGCTAAATCG

wrm 23175 4

2 21925 TP 415.203 415.217 1/u g 15

SEQ ID No. 186

TGGTCTGCTAAATCG

wrm 23175 4

2 22854 CP 708.793 708.810 1/u g 18

SEQ ID No. 187

AAACTTGTAGTTTGTAGT

wrm 23175 4

2 22166 TP 486.479 486.496 1/u g 18

SEQ ID No. 188

AAACTTGTAGTTTGTAGT

wrm 23179 4

2 24763 CN 1373.569 1373.584 1/u g 16

SEQ ID No. 189

ATTTAGCAGACCCAAA

wrm 23179 4

2 22165 TN 486.461 486.476 1/u g 16

SEQ ID No. 190

ATTTAGCAGACCCAAA

wrm 23179 4

2 24763 CN 1373.554 1373.572 1/u g 19

SEQ ID No. 191

AAACTACAAATTTTCGATTT

wrm 23179 4

2 21926 TN 415.212 415.230 1/u g 19

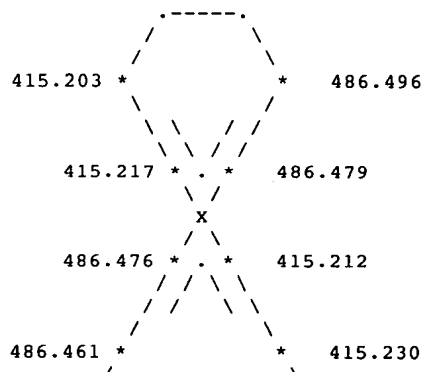
SEQ ID No. 192

AAACTACAAATTTTCGATTT

Found L/U DA AB - CD Connectron pair for 23175 and 23179 with a lifetime = 15 x 16 = 240

.005 .003

415.203 415.217 486.479 486.496 --- 486.461 486.476 415.212 415.230



# Description of an asymmetric lower-upper connectron pair in *H. sapiens*

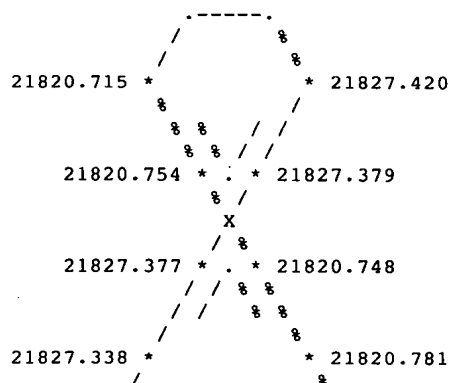
5 The connectron 383992 has a C1-T1 binding length of 39 bases and  
a C2-T2 binding length of 41 bases. The shorter of the two  
matches at 39 bases produces the lifetime for this connectron.  
The connectron 383993 has a C1-T1 binding length of 40 bases and  
a C2-T2 binding length of 34 bases. The shorter of the two  
0 matches at 34 bases produces the lifetime for this connectron.  
The lifetime of this pair of dominant - anti-dominant  
connectrons as shown in figure 9c is 1326.

	genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
15	sequence of match										
20	hsd	383992	920	19	756303	CP	21789.055	21789.092	u/d	g	39
25	<u>SEQ ID No. 193</u>										
	AGCCCGAGCCCCACCTCTCCCTTAGGGACCTCCGCCAC										
30	hsd	383992	920	19	756563	TP	21820.715	21820.754	u/d	g	39
	<u>SEQ ID No. 194</u>										
	AGCCCGAGCCCCACCTCTCCCTTAGGGACCTCCGCCAC										
35	hsd	383992	920	19	756303	CP	21789.080	21789.121	u/d	g	41
	<u>SEQ ID No. 195</u>										
	ACCTCCGCCCCACCCTACCCTCAAGCCAGGATGCCCGGAGCG										
	hsd	383992	920	19	756615	TP	21827.379	21827.420	u/d	g	41
40	<u>SEQ ID No. 196</u>										
	ACCTCCGCCCCACCCTACCCTCAAGCCAGGATGCCCGGAGCG										
-----											
45	hsd	383993	920	19	756433	CN	21808.781	21808.820	u/d	g	40
	<u>SEQ ID No. 197</u>										
	CCTAAGGGAGAGGTGGGGCTCGGGCTGAATCCCTCGTTGG										
	hsd	383993	920	19	756614	TN	21827.338	21827.377	u/d	g	40
50	<u>SEQ ID No. 198</u>										
	CCTAAGGGAGAGGTGGGGCTCGGGCTGAATCCCTCGTTGG										
	hsd	383993	920	19	756433	CN	21808.740	21808.773	u/d	g	34
	<u>SEQ ID No. 199</u>										
	GCTCCGGGCATCCTGGCTTGAGGGTAGAGTGGGC										
55	hsd	383993	920	19	756564	TN	21820.748	21820.781	u/d	g	34
	<u>SEQ ID No. 200</u>										
	GCTCCGGGCATCCTGGCTTGAGGGTAGAGTGGGC										

Found L/U DA AB - CD Connectron pair for 383992 and 383993 with a lifetime = 39 X 34 = 1326

0.006 0.002

21820.715 21820.754 21827.379 21827.420 --- 21827.338 21827.377 21820.748 21820.781



### Description of an asymmetric lower-upper connectron pair in *A. thaliana*

The connectron 188312 has a C1-T1 binding length of 20 bases and a C2-T2 binding length of 30 bases. The shorter of the two matches at 20 bases produces the lifetime for this connectron.

The connectron 188397 has a C1-T1 binding length of 30 bases and a C2-T2 binding length of 16 bases. The shorter of the two matches at 16 bases produces the lifetime for this connectron.

The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 9c is 340.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
ath	188312	18	4	269631	CP	5320.517	5320.536	u/d	g	20

#### SEQ ID No. 201

TTGTAGACGTATGGTGGTGG

ath	188312	18	4	269507	TP	5311.160	5311.179	u/d	g	20
-----	--------	----	---	--------	----	----------	----------	-----	---	----

#### SEQ ID No. 202

TTGTAGACGTATGGTGGTGG

ath	188312	18	4	269631	CP	5320.519	5320.548	u/d	g	30
-----	--------	----	---	--------	----	----------	----------	-----	---	----

#### SEQ ID No. 203

GTAGACGTATGGTGGTGGGAGACTTGTA

ath	188312	18	4	269890	TP	5340.361	5340.390	u/d	g	30
-----	--------	----	---	--------	----	----------	----------	-----	---	----

#### SEQ ID No. 204

GTAGACGTATGGTGGTGGGAGACTTGTA

ath	188397	18	4	269741	CN	5324.883	5324.921	u/d	g	39
-----	--------	----	---	--------	----	----------	----------	-----	---	----

SEQ ID No. 205

GCTCTCCACCACCACCATACTACAGTCCATCTCCAAAGG

ath 188397 18 4 269881 TN 5340.322 5340.360 u/d g 39

SEQ ID No. 206

GCTCTCCACCACCACCATACTACAGTCCATCTCCAAAGG

ath 188397 18 4 269741 CN 5324.867 5324.882 u/d g 16

SEQ ID No. 207

CCACCATACGTCTACA

ath 188397 18 4 269509 TN 5311.176 5311.191 u/d g 16

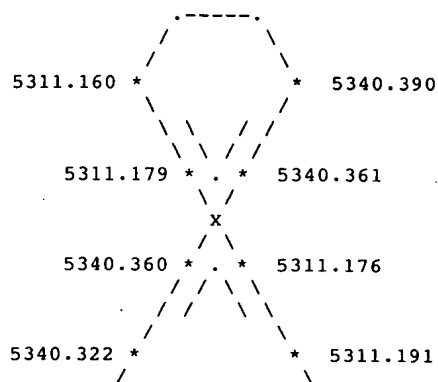
SEQ ID No. 208

CCACCATACGTCTACA

Found L/U DA AB - CD Connectron pair for 188312 and 188397 with a lifetime = 20 X 16 = 320

0.003 0.001

5311.160 5311.179 5340.361 5340.390 --- 5340.322 5340.360 5311.176 5311.191

**Description of an asymmetric left-right connectron pair in E. coli**

The connectron 3707 has a C1-T1 binding length of 21 bases and a C2-T2 binding length of 19 bases. The shorter of the two matches at 19 bases produces the lifetime for this connectron.

The connectron 3763 has a C1-T1 binding length of 42 bases and a C2-T2 binding length of 37 bases. The shorter of the two matches at 37 bases produces the lifetime for this connectron.

The lifetime of this pair of dominant - dominant connectrons as shown in figure 10a is 703.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
eco	3707	1	1	3906	CN	2338.350	2338.370	l/r g	21	

SEQ ID No. 209

AACGCCTTATCCGGCCTACGG

eco	3707	1	1	689	TP	374.169	374.189	l/r g	21
-----	------	---	---	-----	----	---------	---------	-------	----

SEQ ID No. 210

AACGCCTTATCCGGCCTACGG

eco	3707	1	1	3906	CN	2338.380	2338.398	l/r g	19
-----	------	---	---	------	----	----------	----------	-------	----

SEQ ID No. 211

GTAGGCCTGATAAGACGCG

eco	3707	1	1	707	TN	376.619	376.637	l/r g	19
-----	------	---	---	-----	----	---------	---------	-------	----

SEQ ID No. 212

GTAGGCCTGATAAGACGCG

eco	3763	1	1	709	CP	376.712	376.753	l/r g	42
-----	------	---	---	-----	----	---------	---------	-------	----

SEQ ID No. 213

GTAGGCCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

eco	3763	1	1	690	TN	374.152	374.193	l/r g	42
-----	------	---	---	-----	----	---------	---------	-------	----

SEQ ID No. 214

GTAGGCCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

eco	3763	1	1	709	CP	376.717	376.753	l/r g	37
-----	------	---	---	-----	----	---------	---------	-------	----

SEQ ID No. 215

CCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

eco	3763	1	1	706	TP	376.617	376.653	l/r g	37
-----	------	---	---	-----	----	---------	---------	-------	----

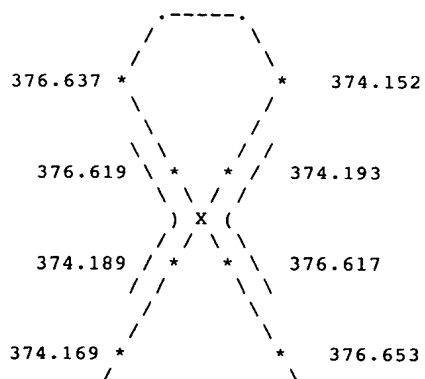
SEQ ID No. 216

CCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

Found L/R DD AB - CD Connectron pair for 3707 and 3763 with a lifetime = 19 x 37 = 703

.004 .002

374.169 374.189 376.619 376.637 --- 374.152 374.193 376.617 376.653



# **Description of an asymmetric left-right connectron pair in *S. cerevisiae***

The connectron 6834 has a C1-T1 binding length of 105 bases and a C2-T2 binding length of 38 bases. The shorter of the two matches at 38 bases produces the lifetime for this connectron. The connectron 6944 has a C1-T1 binding length of 152 bases and a C2-T2 binding length of 143 bases. The shorter of the two matches at 143 bases produces the lifetime for this connectron. The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 10c is 5434.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match									
yst 6834	7	7	10928 CN	111.321	111.425	1/r g		105	

SEQ ID No. 217 CGGTGTTAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTG  
GAAGCTGAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAAC  
ATATA  
yst 6834 3 3 2988 TP 84.359 84.463 1/r g 105

SEQ ID No. 218 CGGTGTTAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTG  
GAAGCTGAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAAC  
ATATA  
yst 6834 7 7 10945 CN 111.449 111.486 1/r g 38

SEQ ID No. 219 TCATCTACTAACTAGTATTTACGTTACTAGTATATTAT  
yst 6834 3 3 3500 TN 168.765 168.802 1/r g 38

SEQ ID No. 220 TCATCTACTAACTAGTATTTACGTTACTAGTATATTAT

yst 6944 4 4 5116 CN 645.641 645.792 1/r g 152

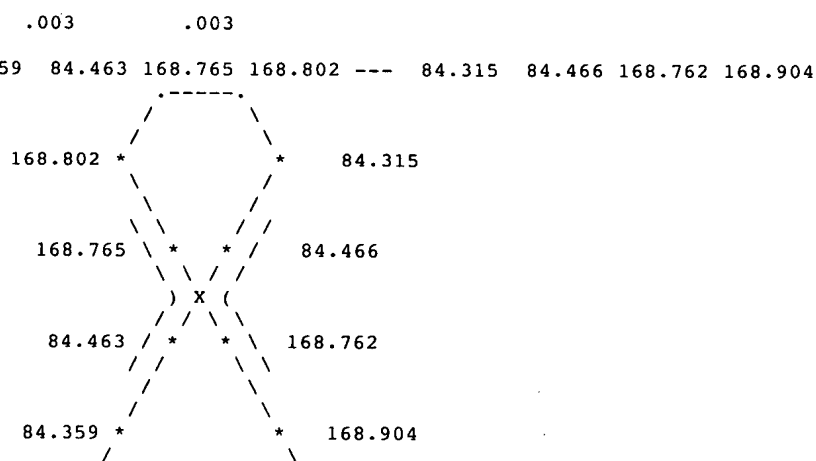
SEQ ID No. 221 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT  
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT  
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA  
AA  
yst 6944 3 3 2991 TP 84.315 84.466 1/r g 152

SEQ ID No. 222 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT  
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT  
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA  
AA  
yst 6944 4 4 5116 CN 645.641 645.783 1/r g 143

SEQ ID No. 223 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT  
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT  
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA  
AA  
yst 6944 3 3 3496 TN 168.762 168.904 1/r g 143

SEQ ID No. 224 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT  
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT  
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA  
AA

Found L/R DA AB - CD Connectron pair for 6834 and 6944 with a lifetime =  $38 \times 143 = 5434$



### Description of an asymmetric left-right connectron pair in *C. elegans*

The connectron 40849 has a C1-T1 binding length of 34 bases and a C2-T2 binding length of 34 bases. The either of the two matches at 34 bases produces the lifetime for this connectron. The connectron 40850 has a C1-T1 binding length of 48 bases and a C2-T2 binding length of 39 bases. The shorter of the two matches at 39 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 10d is 1326.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match				type					
wrm	40849	6	2	51392 CN	13819.470	13819.500	l/r g		34

SEQ ID No. 225 ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT

wrm 40849 6 2 51379 TN 13817.594 13817.630 l/r g 34

SEQ ID No. 226 ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT

wrm 40849 6 2 51392 CN 13819.470 13819.500 l/r g 34

SEQ ID No. 227 ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT

wrm 40849 6 2 51400 TP 13820.550 13820.583 l/r g 34

SEQ ID No. 228 ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT

wrm 40850 6 2 51410 CN 13820.791 13820.840 l/r g 48

SEQ ID No. 229 CAACACACCTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGTT

wrm 40850 6 2 51379 TN 13817.583 13817.630 l/r g 48

SEQ ID No. 230 CAACACACCTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGTT

wrm 40850 6 2 51410 CN 13820.800 13820.840 l/r g 39

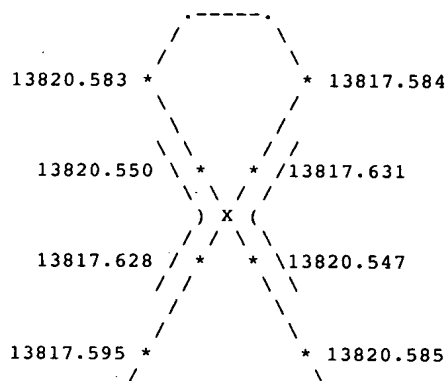
SEQ ID No. 231 CTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGT

wrm 40850 6 2 51400 TP 13820.550 13820.584 l/r g 39

SEQ ID No. 232 CTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGT

Found L/R AD AB - CD Connectron pair for 40849 and 40850 with a lifetime = 34 X 39 = 1326  
.003 .003

13817.595 13817.628 13820.550 13820.583 --- 13817.584 13817.631 13820.547 13820.585



#### Description of an asymmetric left-right connectron pair in *H. sapiens*

The connectron 67620 has a C1-T1 binding length of 38 bases and a C2-T2 binding length of 33 bases. The shorter of the two matches at 33 bases produces the lifetime for this connectron. The connectron 67621 has a C1-T1 binding length of 41 bases and a C2-T2 binding length of 42 bases. The shorter of the two matches at 41 bases produces the lifetime for this connectron. The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 10c is 1353.



genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
hsd	67620	100	1	96091	CN	1705.996	1706.033	l/r	g	38

SEQ ID No. 233

GTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGC

hsd 67620 60

1 78101 TP 218.397 218.434 l/r g 38

SEQ ID No. 234

GTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGC

hsd 67620 100

1 96101 CN 1705.970 1706.002 l/r g 33

SEQ ID No. 235

AGGTCAGGAGATCGAGACCATCCTGGCTAACAC

hsd 67620 60

1 78110 TN 234.341 234.373 l/r g 33

SEQ ID No. 236

AGGTCAGGAGATCGAGACCATCCTGGCTAACAC

hsd 67621 100

1 98781 CN 3142.085 3142.125 l/r g 41

SEQ ID No. 237

CGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCC

hsd 67621 60

1 78101 TP 218.395 218.435 l/r g 41

SEQ ID No. 238

CGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCC

hsd 67621 100

1 98781 CN 3142.052 3142.093 l/r g 42

SEQ ID No. 239

GAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC

hsd 67621 60

1 78110 TN 234.340 234.381 l/r g 42

SEQ ID No. 240

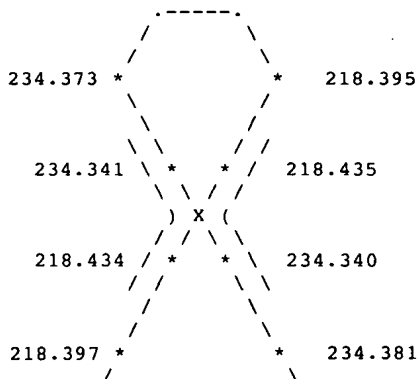
GAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC

Found L/R DA AB - CD Connectron pair for 67620 and 67621 with a lifetime = 33 X 41 = 1353

0.001

0.001

218.397 218.434 234.341 234.373 --- 218.395 218.435 234.340 234.381



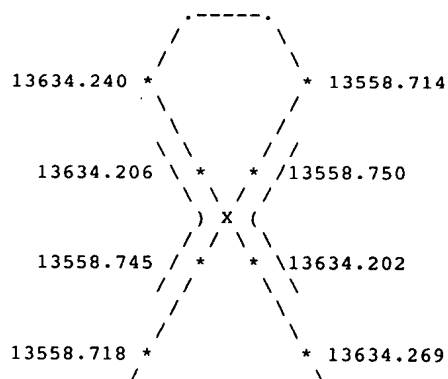
**Description of an asymmetric left-right connectron pair  
in *A. thaliana***

The connectron 5 has a C1-T1 binding length of 28 bases and a C2-T2 binding length of 35 bases. The shorter of the two matches at 28 bases produces the lifetime for this connectron. The connectron 6 has a C1-T1 binding length of 37 bases and a C2-T2 binding length of 68 bases. The shorter of the two matches at 37 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 10d is 1036.

	genome	Connectron id chromosome	contig	(.groups) id type	match start	match stop type of Connectron source of Connectron length of match
15	sequence of match					
20	ath	5	15	3	102175 CN	12540.150 12540.174 l/r g 28
25	<u>SEQ ID No. 241</u>				ATCATCAATGAACTCATTGGCTAAGGT	
30	ath	5	15	3	102902 TN	13558.720 13558.750 l/r g 28
	<u>SEQ ID No. 242</u>				ATCATCAATGAACTCATTGGCTAAGGT	
	ath	5	15	3	102176 CN	12540.184 12540.220 l/r g 35
35	<u>SEQ ID No. 243</u>				ACATTCATTAGTTCTGGAACGTGAATCAAGCAATG	
	ath	5	15	3	103090 TP	13634.210 13634.240 l/r g 35
40	<u>SEQ ID No. 244</u>				ACATTCATTAGTTCTGGAACGTGAATCAAGCAATG	
<hr/>						
	ath	6	15	3	103067 CP	13626.660 13626.700 l/r g 37
45	<u>SEQ ID No. 245</u>				ATGCATCATCAATGAACTCATTGGCTAAGGTGAAGG	
	ath	6	15	3	102902 TN	13558.713 13558.750 l/r g 37
	<u>SEQ ID No. 246</u>				ATGCATCATCAATGAACTCATTGGCTAAGGTGAAGG	
50	ath	6	15	3	103067 CP	13626.624 13626.691 l/r g 68
	<u>SEQ ID No. 247</u>				TTTAACATTCATTAGTTCTGGAACGTGAATCAAGCAATGCATCATCAATG	
55	AATCATTGGCTAAGGT					
	ath	6	15	3	103090 TP	13634.202 13634.270 l/r g 68
	<u>SEQ ID No. 248</u>				TTTAACATTCATTAGTTCTGGAACGTGAATCAAGCAATGCATCATCAATG	
	AATCATTGGCTAAGGT					

Found L/R AD AB - CD Connectron pair for 5 and 6 with a lifetime =  $28 \times 37 = 1036$   
 .005 .004

5 13558.718 13558.745 13634.206 13634.240 --- 13558.714 13558.750 13634.202 13634.269



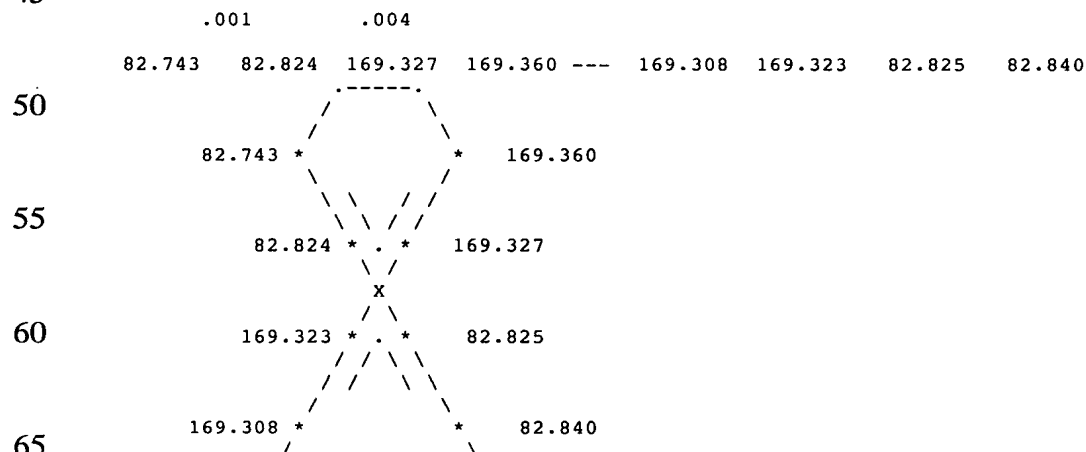
# **Design of an asymmetric lower-upper connectron pair in *S. cerevisiae***

There are many ways to design a pair of connectrons. In this example we have chosen to replace the C1 source and the T1 target of the upper naturally occurring connectron with another sequence. Design of a connectron pair can be accomplished by anyone skilled the art by modifying and/or replacing any of the sources and targets in the four positions of either a lower-upper or a left-right connectron pair. A totally synthetic pair of dominant - anti-dominant connectrons could also be designed de-novo.

The connectron 5441 has a C1-T1 binding length of 82 bases and a C2-T2 binding length of 35 bases. The shorter of the two matches at 34 bases produces the lifetime for this connectron. The connectron 5500 has a C1-T1 binding length of 16 bases and a C2-T2 binding length of 16 bases. Either of the two matches at 16 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 9c is 544.

	genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
5	sequence of match									
10	yst	5441	3	3	2944 CP	84.112	84.193	l/u g		82
15	SEQ ID No. 249 ATACGTTTGAAGAAATCACTTTATGGATTGAAACAAAGTGGAGCGAACTG GTACGAACTATCAAATCATACCTGATAAAAC yst 5441 3 3 2901 TP 82.743 82.824 l/u g 82									
20	SEQ ID No. 250 ATACGTTTGAAGAAATCACTTTATGGATTGAAACAAAGTGGAGCGAACTG GTACGAACTATCAAATCATACCTGATAAAAC yst 5441 3 3 2965 CP 84.195 84.228 l/u g 34									
25	SEQ ID No. 251 GAAACGTGACGGTACTCATAAAGCTAGATTTGTT yst 5441 3 3 3529 TP 169.327 169.360 l/u g 34									
	SEQ ID No. 252 GAAACGTGACGGTACTCATAAAGCTAGATTTGTT									
30	yst	5500	3	3	3387 CN	151.534	151.549	l/u g		16
	SEQ ID No. 253 TAATTGTTGGGATTCC yst 5500 3 3 3526 TN 169.308 169.323 l/u g 16									
35	SEQ ID No. 254 TAATTGTTGGGATTCC yst 5500 3 3 3387 CN 151.516 151.531 l/u g 16									
40	SEQ ID No. 255 AAAGGCTATAATATTA yst 5500 3 3 2905 TN 82.825 82.840 l/u g 16									
	SEQ ID No. 256 AAAGGCTATAATATTA									

45 Found L/U DA AB - CD Connectron pair for 5441 and 5500 with a lifetime = 34 X 16 = 544



### Design of an asymmetric lower-upper connectron pair in *H. sapiens*

There are many ways to design a pair of connectrons. In this example we have chosen to replace the C1 source and the T1

target of the right naturally occurring connectron with another sequence. Design of a connectron pair can be accomplished by anyone skilled the art by modifying and/or replacing any of the sources and targets in the four positions of either a lower-  
 5 upper or a left-right connectron pair. A totally synthetic pair of anti-dominant - dominant connectrons could also be designed de-novo.

10 The connectron 395760 has a C1-T1 binding length of 32 bases and a C2-T2 binding length of 32 bases. Either of the two matches at 32 bases produces the lifetime for this connectron. The connectron 395762 has a C1-T1 binding length of 40 bases and a C2-T2 binding length of 39 bases. The shorter of the two  
 15 matches at 39 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 10c is 1248.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match				type					
hsd 395760 920		19 747775 CP 17572.332			17572.363	1/r g			32
<u>SEQ ID No. 257</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395760 922		19 765474 TN 27988.178 27988.209			1/r g				32
<u>SEQ ID No. 258</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395760 920		19 747777 CP 17572.369 17572.400			1/r g				32
<u>SEQ ID No. 259</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395760 922		19 765567 TP 28004.852 28004.883			1/r g				32
<u>SEQ ID No. 260</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395762 920		19 747819 CP 17573.447 17573.486			1/r g				40
<u>SEQ ID No. 261</u>		CCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGACCCC							
hsd 395762 922		19 765474 TN 27988.176 27988.215			1/r g				40
<u>SEQ ID No. 262</u>		CCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGACCCC							
hsd 395762 920		19 747823 CP 17573.520 17573.557			1/r g				39
<u>SEQ ID No. 263</u>		GGCCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGGT							
hsd 395762 922		19 765567 TP 28004.848 28004.887			1/r g				39
<u>SEQ ID No. 264</u>		GGCCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGGT							

Found L/R AD AB - CD Connectron pair for 395760 and 395762 with a lifetime = 32 X 39 = 1248

0.006 0.004

27988.178 27988.209 28004.852 28004.883 --- 27988.176 27988.215 28004.848 28004.887

